Figure 1.

	Tail				46*	Shaft	66
D 30	MSKRLRV.ED	DFNPVYPYGY	ARN.QNIPFL	TPPFVSSDGF	.KNFPPGV	LSLKLADPIA	ITNGDVSLKV
C 5	M.KRARPSED	TFNPVYPYDT	ETGPPTVPFL	TPPFVSPNGF	.QESPPGV	LSLRLSEPLV	TSNGMLALKM
D 9	MSKRLRV.ED	DFNPVYPYGY	ARN.QNIPFL	TPPFVSSDGF	.QNFPPGV	LSLKLADPIA	IVNGNVSLKV
D 17	MSKRLRV.ED	DFNPVYPYGY	ARN.QNIPFL	TPPFVSSDGF	.KNFPPGV	LSLKLADPIT	IANGDVSLKV
B 3	MAKRARL.ST	SFNPVYPYED	ESSSQH.PFI	NPGFISPDGF	TQ.SPNGV	LSLKCVNPLT	TASGSLQLKV

							135
30	GGGLTVEQD.	....	....	....	....	....	....
5	GNGLSL.DEA	GNLTSQNVTT	VSPPLKKTKS	NINLEISAPL	TVTSEALTVA	AAAPLMVAGN	TLTMQSQAPL
9	GGGLTL.QDG	T.........	....	....	....	....	....
17	GGGLTL.QE.	....	....	....	....	....	....
3	GSGLTV.D..	....	....	....	....	....	....

							205
30	....	....	....	....SGNLSV	NPKAPLQ...	....	.VGTDKKLEL
5	TVHDSKLSIA	TQGPLTVSEG	KLALQTSGPL	TTTDSSTLTI	TASPPLTTAT	GSLGIDLKEP	IYTQNGKLGL
9	....	....	....	.....GKLTV	NADPPLQ...	....	.LTNN.KLGI
17	....	....	....	.....GSLTV	DPKAPLQ...	....	.LANNKKLEL
3	....	....	....	....	......TT..	..DGSLEENI	

							275
30	ALAPPFDVRD	..NKLAILVG	DGLKVIDRSI	SDLPGLLNY.	....	....	....
5	KYGAPLHVTD	DLNTLTVATG	PGVTINNTSL	QTKVTGALGF	DSQGNMQLNV	AGGLRIDSQN	RRLILDVSYP
9	ALDAPFDVID	..NKLTLLAG	HGLSII.TKE	TSTLPGLRN.	....	....	....
17	VYVDPFEVSA	..NKLSLKVG	HGLKILDDKS	AGGLKDLIG.	....	....	....
3	KVNTPLTKSN	HSINL..PIG	NGLQIEQNKL	CS........	....	....	....

							345
30	....	....	....	....	....	....	LVVLTGKGIG
5	FDAQNQLNLR	LGQGPLFINS	AHNLDINYNK	GLYLFTASNN	SKKLEVNLST	AKGLMFDATA	IAINAGDGLE
9	....	....	....	....	....	........T	LVVLTGKGIG
17	....	....	....	....	....	........K	LVVLTGKGIG
3	....	....	....	....	....	....	

				400*		410
30	NEELKNDDGS	NKGVGLCVRI	G.E.......	....GGGLTF	DDKGYLVAWN	NKHDIRT	LWTTLDPSPN
5	FG..SPNAPN	TNPLKTKIGH	GLEFDSNKAM	VPKLGTGLSF	DSTGAITVGN	KNNDKLT	LWTTPAPSPN
9	TESTDNGG..	..TVCRV..	G.E.......	....GGGLSF	NNDGDLVAFN	KKEDKRT	LWTTPDTSPN
17	TENLQNTDGS	SRGIGISVRA	....	....REGLTF	DNDGYLVAWN	PKYDTRT	LWTTPDTSPN
3	....	....	....	..KLGNGLTF	DSSNSIALKN	N.....T	LWTGPKPEAN

						471
30	CKID...IEK	DSKLTLVLTK	CGSQILANVS	LIIVNGKFKI	LNNKTDP.SL	PKSFNIKLLF	DQNGVLLENS
5	CRLN...AEK	DAKLTLVLTK	CGSQILATVS	VLAV.K....	.GSLAPISGT	VQSAHLIIRF	DENGVLLNNS
9	CKID...QDK	DSKLTLVLTK	CGSQILANVS	LIVVDGKYKI	INNNTQP..A	LKGFTIKLLF	DENGVLMESS
17	CRID...KEK	DSKLTLVLTK	CGSQILANVS	LIVVSGKYQY	IDHATNP..T	LKSFKIKLLF	DNKGVLLPSS
3	CIIEYGKQNP	DSKLTLILVK	NGGIVNGYVT	LMGASDYVNT	LFKNKNV...	..SINVELYF	DATGHILPDS

						526
30	N........I	EKQYLNFRSG	DSILPEPYKN	AIGFMPNLLA	YAKATTDQSK	IY...ARNTI	YGNIYLDNQP
5	F........L	DPEWNFRNG	ILTEGTAYTN	AVGFMPNLSA	YPKSHGK.T.	.....AKSNI	VSQVYLNGDK
9	N........L	GKSYWNFRNE	NSIMSTAYEK	AIGFMPNLVA	YPKPTAG.SK	KY...ARDIV	YGNIYLGGKP
17	N........L	DSTYWNFRSD	NLTVSEAYKN	AVEFMPNLVA	YPKPTTG.SK	KY...ARDIV	YGNIYLGGLA
3	SSLKTDLELK	YKQTADF...	........S	ARGFMPSTTA	YPFVLPN.AG	TH...NENYI	FGQCYYKASD

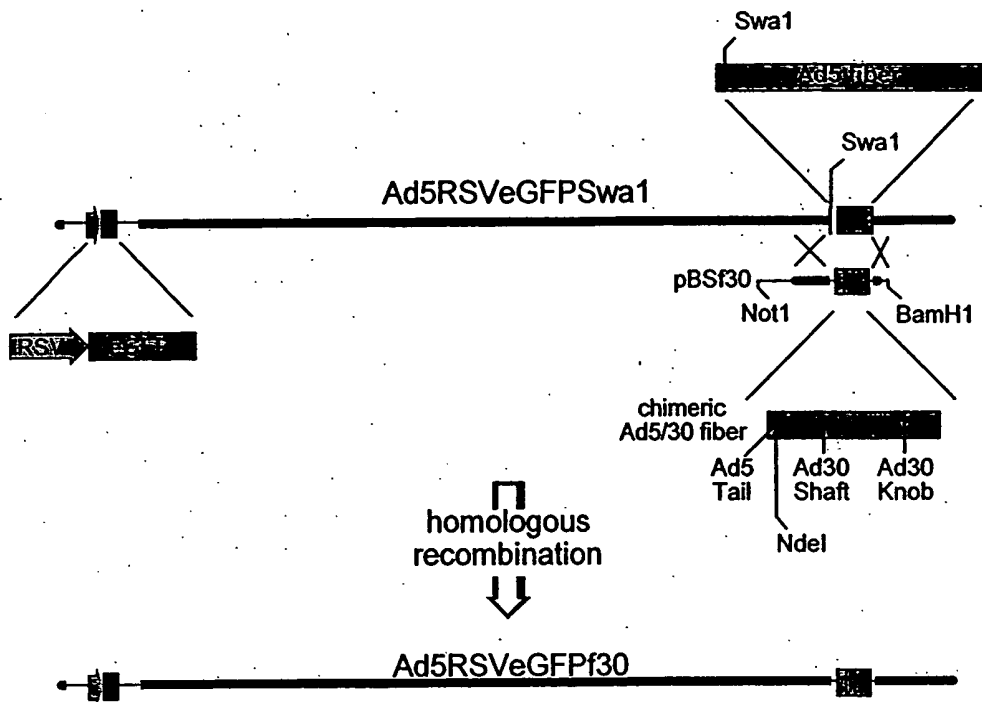|						582*	
30	YN..PVVIKI	TFNNEAD...	....SAYSIT	FNYSWTKD.Y	DNIPFDSTSF	TFSYIAQE	
5	TK..PVTLTI	TLNGTQETGD	TT.PSAYSMS	FSWDWSGHNY	INEIPATSSY	TFSYIAQE	**Knob**
9	DQ..PVTIKT	TFNQETG...	....CEYSIT	FDFSWAKT.Y	VNVEFETTSF	TFSYIAQE	
17	YQ..PVVIKV	TFNEEAD...	....SAYSIT	FEFVWNKE.Y	ARVEFETTSF	TFSYIAQQ	
3	GALFPLEVTV	MLNKRLPDSR	TSYVMTFLWS	LNAGLAPET.	TQATLITSPF	TFSYIREDD	

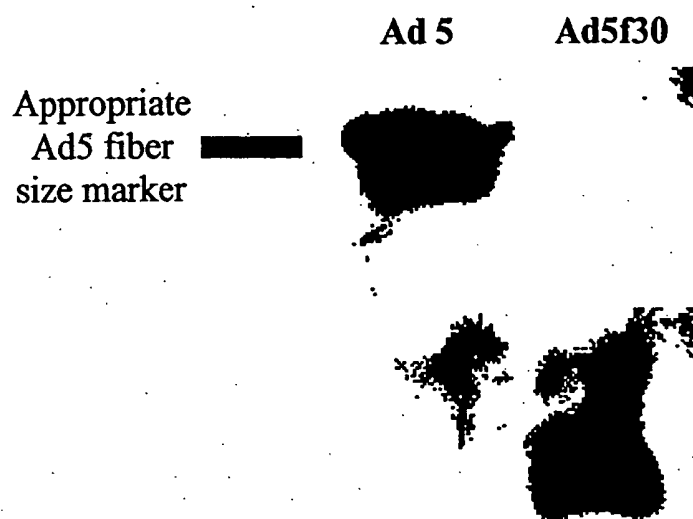* numbers refer to Ad5 amino acid sequence

Figure 2.

Amino Acids within Ad5 fiber **Important** and <u>**Critical**</u> for CAR Binding

<u>Binds CAR?</u>

	401 (Ad5)		473 (Ad5)
D 30	LWTTLDPSPNCKID	?	30 GDSILPEPYKNAIGFMPN
C 5	LWTTPAP<u>SP</u>NCRLN	Yes	5 LDPE<u>Y</u>WNFRNGD<u>L</u>TEGTA
C 2	LWTTPDPSPNCRIH	Yes	2 LKKHYWNFRNGNSTNANP
D 9	LWTTPDTSPNCKID	Yes/No	9 LGKSYWNFRNENSIMSTA
D 17	LWTTPDTSPNCKID	Yes	17 LDSTYWNFRSDNLTVSEA
B 3	LWTGPKPEANCIIE	No	3 . . . . .SARGFMPS

Figure 3.

Figure 4.

Ad 5   Ad5f30

Appropriate
Ad5 fiber
size marker

Figure 5a.

Figure 5b.

% eGFP positive cells

Figure 6.

Figure 7a.

□ Ad5
■ Ad5f30

% eGFP positive cells

Figure 7b.

□ Ad5
■ Ad5f30